

What is claimed is:

1. An isolated nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1, the complement of SEQ ID NO:1, SEQ ID NO:3, the complement of SEQ ID NO:3, SEQ ID NO:5, the complement of SEQ ID NO:5, SEQ ID NO:7, the complement of SEQ ID NO:7, SEQ ID NO:9, the complement of SEQ ID NO:9, SEQ ID NO:11, the complement of SEQ ID NO:11, SEQ ID NO:13, and the complement of SEQ ID NO:13.
2. An isolated nucleic acid at least 95% identical to a sequence of a nucleic acid of claim 1 as determined by analysis with a sequence comparison algorithm or by visual inspection.
3. An isolated nucleic acid at least 90% identical to a sequence of a nucleic acid of claim 1 as determined by analysis with a sequence comparison algorithm or by visual inspection.
4. An isolated nucleic acid at least 80% identical to a sequence of a nucleic acid of claim 1 as determined by analysis with a sequence comparison algorithm or by visual inspection.
5. An isolated nucleic acid at least 70% identical to a sequence of a nucleic acid of claim 1 as determined by analysis with a sequence comparison algorithm or by visual inspection.
6. An isolated nucleic acid at least 60% identical to a sequence of a nucleic acid of claim 1 as determined by analysis with a sequence comparison algorithm or by visual inspection.
7. An isolated nucleic acid at least 50% identical to a sequence of a nucleic acid of claim 1 as determined by analysis with a sequence comparison algorithm or by visual inspection.
8. An isolated nucleic acid that hybridizes to a nucleic acid of claim 1 under conditions of high stringency.
9. An isolated nucleic acid that hybridizes to a nucleic acid of claim 1 under conditions of moderate stringency.
10. An isolated nucleic acid that hybridizes to a nucleic acid of claim 1 under conditions of low stringency.

11. The nucleic acid of claim 1, wherein the nucleotide sequence selected has the nucleotide sequence set forth as SEQ ID NO:1.
12. The nucleic acid of claim 1, wherein the nucleotide sequence selected has the nucleotide sequence set forth as the complement of SEQ ID NO:1.
- 5 13. The nucleic acid of claim 1, wherein the nucleotide sequence selected has the nucleotide sequence set forth as SEQ ID NO:3.
14. The nucleic acid of claim 1, wherein the nucleotide sequence selected has the nucleotide sequence set forth as the complement of SEQ ID NO:3.
- 10 15. The nucleic acid of claim 1, wherein the nucleotide sequence selected has the nucleotide sequence set forth as SEQ ID NO:5.
16. The nucleic acid of claim 1, wherein the nucleotide sequence selected has the nucleotide sequence set forth as the complement of SEQ ID NO:5.
17. The nucleic acid of claim 1, wherein the nucleotide sequence selected has the nucleotide sequence set forth as SEQ ID NO:7.
- 15 18. The nucleic acid of claim 1, wherein the nucleotide sequence selected has the nucleotide sequence set forth as the complement of SEQ ID NO:7.
19. The nucleic acid of claim 1, wherein the nucleotide sequence selected has the nucleotide sequence set forth as SEQ ID NO:9.
- 20 20. The nucleic acid of claim 1, wherein the nucleotide sequence selected has the nucleotide sequence set forth as the complement of SEQ ID NO:9.
21. The nucleic acid of claim 1, wherein the nucleotide sequence selected has the nucleotide sequence set forth as SEQ ID NO:11.
22. The nucleic acid of claim 1, wherein the nucleotide sequence selected has the nucleotide sequence set forth as the complement of SEQ ID NO:11.
- 25 23. The nucleic acid of claim 1, wherein the nucleotide sequence selected has the nucleotide sequence set forth as SEQ ID NO:13.
24. The nucleic acid of claim 1, wherein the nucleotide sequence selected has the nucleotide sequence set forth as the complement of SEQ ID NO:13.
25. An expression vector comprising: the nucleic acid of claim 1.

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26. The expression vector of claim 25 further comprising an expression control nucleotide sequence.
27. A host cell transformed with the nucleic acid of claim 1.
28. The host cell of claim 27 selected from the group consisting of a bacterium, a
5 fungus, a plant or an animal cell.
29. A host cell comprising the expression vector of claim 23.
30. The host cell of claim 29 selected from the group consisting of a bacterium, a
fungus, a plant or an animal cell.
31. An isolated nucleic acid comprising a nucleotide sequence encoding a polypeptide
10 having an amino acid sequence selected from the group consisting of SEQ ID NO:2,
SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and
SEQ ID NO:14.
32. The nucleic acid of claim 31 encoding the polypeptide having the amino acid
sequence set forth as SEQ ID NO:2.
- 15 33. The nucleic acid of claim 31 encoding the polypeptide having the amino acid
sequence set forth as SEQ ID NO:4.
34. The nucleic acid of claim 31 encoding the polypeptide having the amino acid
sequence set forth as SEQ ID NO:6.
35. The nucleic acid of claim 31 encoding the polypeptide having the amino acid
20 sequence set forth as SEQ ID NO:8.
36. The nucleic acid of claim 31 encoding the polypeptide having the amino acid
sequence set forth as SEQ ID NO:10.
37. The nucleic acid of claim 31 encoding the polypeptide having the amino acid
sequence set forth as SEQ ID NO:12.
- 25 38. The nucleic acid of claim 31 encoding the polypeptide having the amino acid
sequence set forth as SEQ ID NO:14.
39. An expression vector comprising the isolated nucleic acid molecule of claim 31.
40. The expression vector of claim 39 further comprising an expression control
nucleotide sequence.

41. A host cell transformed with the nucleic acid molecule of claim 31.
42. The host cell of claim 41 selected from the group consisting of a bacterium, a fungus, a plant or an animal cell.
43. A host cell comprising the expression vector of claim 39.
- 5 44. The host cell of claim 43 selected from the group consisting of a bacterium, a fungus, a plant or an animal cell.
45. An isolated nucleic acid comprising a nucleotide sequence encoding a polypeptide having at least thirty contiguous amino acids of a protein having an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ
10 ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14.
46. The nucleic acid of claim 45 comprising a nucleotide sequence encoding a polypeptide having at least thirty contiguous amino acids of SEQ ID NO:2.
47. The phytase protein of claim 45 having an amino acid sequence comprising SEQ ID NO:2.
- 15 48. The nucleic acid of claim 45 comprising a nucleotide sequence encoding a polypeptide having at least thirty contiguous amino acids of SEQ ID NO:4.
49. The phytase protein of claim 45 having an amino acid sequence comprising SEQ ID NO:4.
50. The nucleic acid of claim 45 comprising a nucleotide sequence encoding a
20 polypeptide having at least thirty contiguous amino acids of SEQ ID NO:6.
51. The phytase protein of claim 45 having an amino acid sequence comprising SEQ ID NO:6.
52. The nucleic acid of claim 45 comprising a nucleotide sequence encoding a polypeptide having at least thirty contiguous amino acids of SEQ ID NO:8.
- 25 53. The phytase protein of claim 45 having an amino acid sequence comprising SEQ ID NO:8.
54. The nucleic acid of claim 45 comprising a nucleotide sequence encoding a polypeptide having at least thirty contiguous amino acids of SEQ ID NO:10.

55. The phytase protein of claim 45 having an amino acid sequence comprising SEQ ID NO:10.
56. The nucleic acid of claim 45 comprising a nucleotide sequence encoding a polypeptide having at least thirty contiguous amino acids of SEQ ID NO:12.
- 5 57. The phytase protein of claim 45 having an amino acid sequence comprising SEQ ID NO:12.
58. The nucleic acid of claim 45 comprising a nucleotide sequence encoding a polypeptide having at least thirty contiguous amino acids of SEQ ID NO:14.
- 10 59. The phytase protein of claim 45 having an amino acid sequence comprising SEQ ID NO:14.
60. An expression vector comprising the nucleic acid of claim 45.
61. The expression vector of claim 60 further comprising an expression control nucleotide sequence.
62. A host cell transformed with the nucleic acid of claim 45.
- 15 63. The host cell of claim 62 selected from the group consisting of a bacterium, a fungus, a plant or an animal cell.
64. A host cell comprising the expression vector of claim 60.
65. The host cell of claim 64 selected from the group consisting of a bacterium, a fungus, a plant or an animal cell.
- 20 66. An isolated phytase protein comprising a polypeptide having at least thirty contiguous amino acids of a protein having an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14.
- 25 67. The phytase protein of claim 66 comprising a polypeptide having at least 30 contiguous amino acids of SEQ ID NO:2.
68. The phytase protein of claim 66 having an amino acid sequence comprising SEQ ID NO:2.
69. The phytase protein of claim 33 comprising a polypeptide having at least 30 contiguous amino acids of SEQ ID NO:4.

70. The phytase protein of claim 66 having an amino acid sequence comprising SEQ ID NO:4.
71. The phytase protein of claim 66 comprising a polypeptide having at least 30 contiguous amino acids of SEQ ID NO:6.
- 5 72. The phytase protein of claim 66 having an amino acid sequence comprising SEQ ID NO:6.
73. The phytase protein of claim 66 comprising a polypeptide having at least 30 contiguous amino acids of SEQ ID NO:8.
- 10 74. The phytase protein of claim 66 having an amino acid sequence comprising SEQ ID NO:8.
75. The phytase protein of claim 66 comprising a polypeptide having at least 30 contiguous amino acids of SEQ ID NO:10.
76. The phytase protein of claim 66 having an amino acid sequence comprising SEQ ID NO:10.
- 15 77. The phytase protein of claim 66 comprising a polypeptide having at least 30 contiguous amino acids of SEQ ID NO:12.
78. The phytase protein of claim 66 having an amino acid sequence comprising SEQ ID NO:12.
- 20 79. The phytase protein of claim 66 comprising a polypeptide having at least 30 contiguous amino acids of SEQ ID NO:14.
80. The phytase protein of claim 66 having an amino acid sequence comprising SEQ ID NO:14.
81. A nucleic acid expression vector comprising a nucleotide sequence encoding the phytase protein of claim 66.
- 25 82. The expression vector of claim 81 further comprising an expression control nucleotide sequence.
83. A host cell transformed with the nucleotide sequence encoding the phytase protein of claim 66.

84. The host cell of claim 83 selected from the group consisting of a bacterium, a fungus, a plant or an animal cell.
85. A host cell comprising the nucleic acid expression vector of claim 81 and an expression control nucleotide sequence.
- 5 86. The host cell of claim 85 selected from the group consisting of a bacterium, a fungus, a plant or an animal cell.
87. An isolated phytase protein comprising a polypeptide having at least thirty contiguous amino acids of a protein having an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14, wherein the SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14 have at least one conservative amino acid substitution.
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88. The phytase protein of claim 87 comprising a polypeptide having at least 30 contiguous amino acids of SEQ ID NO:4, wherein the polypeptide has at least one conservative amino acid substitution.
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89. The phytase protein of claim 87 comprising the amino acid sequence set forth as SEQ ID NO:4, wherein the amino acid sequence has at least one conservative amino acid substitution.
90. The phytase protein of claim 87 comprising a polypeptide having at least 30 contiguous amino acids of SEQ ID NO:5, wherein the polypeptide has at least one conservative amino acid substitution.
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91. The phytase protein of claim 87 comprising the amino acid sequence set forth as SEQ ID NO:5, wherein the amino acid sequence has at least one conservative amino acid substitution.
92. The phytase protein of claim 87 comprising a polypeptide having at least 30 contiguous amino acids of SEQ ID NO:6, wherein the amino acid sequence has at least one conservative amino acid substitution.
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93. The phytase protein of claim 87 comprising the amino acid sequence set forth as SEQ ID NO:6, wherein the amino acid sequence has at least one conservative amino acid substitution.
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94. The phytase protein of claim 87 comprising a polypeptide having at least 30 contiguous amino acids of SEQ ID NO:7, wherein the amino acid sequence has at least one conservative amino acid substitution.
95. The phytase protein of claim 87 comprising the amino acid sequence set forth as
5 SEQ ID NO:7, wherein the amino acid sequence has at least one conservative amino acid substitution.
96. The phytase protein of claim 87 comprising a polypeptide having at least 30 contiguous amino acids of SEQ ID NO:9, wherein the amino acid sequence has at least one conservative amino acid substitution.
- 10 97. The phytase protein of claim 87 comprising the amino acid sequence set forth as SEQ ID NO:9, wherein the polypeptide sequence has at least one conservative amino acid substitution.
98. The phytase protein of claim 87 comprising a polypeptide having at least 30 contiguous amino acids of SEQ ID NO:10, wherein the amino acid sequence has at
15 least one conservative amino acid substitution.
99. The phytase protein of claim 87 comprising the amino acid sequence set forth as SEQ ID NO:10, wherein the polypeptide sequence has at least one conservative amino acid substitution.
100. A nucleic acid expression vector comprising a nucleotide sequence encoding the
20 phytase protein of claim 87.
101. The expression vector of claim 100 further comprising an expression control nucleotide sequence.
102. A host cell transformed with the nucleotide sequence encoding the phytase protein of claim 87.
- 25 103. The host cell of claim 102 selected from the group consisting of a bacterium, a fungus, a plant or an animal cell.
104. A host cell comprising the nucleic acid expression vector of claim 86.
105. The host cell of claim 104 selected from the group consisting of a bacterium, a fungus, a plant or an animal cell.
- 30 106. A nucleic acid expression vector comprising:

FOOTNOTES

- (a) a nucleotide sequence encoding a polypeptide having at least thirty contiguous amino acids of a protein having an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14; and
- 5 (b) an expression control nucleotide sequence.
107. The nucleic acid expression vector of claim 106, wherein the expression control nucleotide sequence is a constitutive promoter.
108. The nucleic acid expression vector of claim 106, wherein the expression control nucleotide sequence is a tissue-specific promoter.
- 10 109. The nucleic acid expression vector of claim 106, wherein the nucleotide sequence of (a) further comprises a nucleotide sequence encoding a signal peptide.
110. The nucleic acid expression vector of claim 109, wherein the signal peptide is the PR protein PR-S signal peptide from tobacco.
111. A method of improving the nutritional value of a phytate-containing foodstuff, the method comprising contacting the phytate-containing foodstuff with a substantially pure phytase enzyme having an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14, the phytase enzyme catalyzing the liberation of inorganic phosphate from the phytate-containing foodstuff, thereby improving the nutritive value of the contacted foodstuff.
- 15 20 112. The method of claim 111, wherein the phytase enzyme is produced by a recombinant expression system, where in the expression of the phytase-encoding nucleic acid results in the production of the phytase enzyme.
113. The method of claim 111, wherein the liberation of the inorganic phosphate from the phytate in the phytate-containing foodstuff occurs prior to the ingestion of the phytate-containing foodstuff by a recipient organism.
- 25 114. The method of claim 111, wherein the liberation of the inorganic phosphate from the phytate in the phytate-containing foodstuff occurs after the ingestion of the phytate-containing foodstuff by a recipient organism.

115. The method of claim 111, wherein the liberation of the inorganic phosphate from the phytate in the phytate-containing foodstuff occurs in part prior to, and in part after, the ingestion of the phytate-containing foodstuff by a recipient organism.

116. A method to produce an animal feed comprising:

- 5 (a) transforming a plant, plant part or plant cell with the nucleic acid expression vector of claim 86;
- (b) culturing the plant, plant part or plant cell under conditions in which the phytase protein is expressed; and
- 10 (c) converting the plant, plant parts or plant cell into a composition suitable for animal feed.

117. The method of claim 116, wherein in the animal is a monogastric animal.

118. The method of claim 116, wherein the animal is a ruminant.

119. A non-human transgenic organism comprising a heterologous nucleic acid encoding a polypeptide having at least thirty contiguous amino acids of a protein having an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14.

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120. The non-human transgenic organism of claim 119 that is a plant.

121. The plant according to claim 120, wherein the phytase amino acid is expressed in a seed.

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122. A method of producing a substantially purified phytase protein, the method comprising:

- (a) expressing in a cell a phytase a polypeptide having at least thirty contiguous amino acids of a protein having an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14; and
- 25 (b) recovering the phytase protein.

123. The method of claim 122, wherein the cell is a prokaryotic cell.

124. The method of claim 122, wherein the cell is a eukaryotic cell.

30 125. The method of claim 122, wherein the phytase protein is glycosylated.

126. A method of increasing resistance of a phytase polypeptide to enzymatic inactivation in a digestive system of an animal, the method comprising glycosylating the phytase polypeptide.

127. The method of claim 126, wherein glycosylation is N-linked glycosylation.

5 128. The method of claim 126, wherein the phytase polypeptide is glycosylated as a result of *in vivo* expression in a eukaryotic cell.

129. The method of claim 128, wherein the eukaryotic cell is a fungal cell.

130. The method of claim 129, wherein the eukaryotic cell is a plant cell.

131. The method of claim 129, wherein the eukaryotic cell is a mammalian cell.

10 132. A feed composition comprising:

(a) a plant, plant part, or plant cell expressing a polypeptide having at least thirty contiguous amino acids of a protein having an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14; and

15 (b) a phytate-containing foodstuff.

133. The feed composition of claim 132, wherein the plant part is a seed or portion thereof.

134. A feed composition comprising:

20 (a) a substantially purified phytase protein having at least thirty contiguous amino acids of a protein having an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14; and

(b) a phytate-containing foodstuff.

135. The composition of claim 134 manufactured in pellet form.

25 136. The composition of claim 135 produced using polymer coated additives.

137. The composition of claim 134 having a substantially purified phytase protein in granulate form.

138. The composition of claim 134 produced by spray drying.

30 139. An antibody or fragment thereof that specifically recognizes an epitope contained in an amino acid sequence selected from the group consisting of SEQ ID

NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14.

140. The antibody or fragment thereof of claim 139, wherein the antibody is a polyclonal antibody.

5 141. The antibody or fragment thereof of claim 139, wherein the antibody is a monoclonal antibody.

142. A method of generating a variant comprising:

10 (a) obtaining a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NO:1, the complement of SEQ ID NO:1, SEQ ID NO:3, the complement of SEQ ID NO:3, SEQ ID NO:5, the complement of SEQ ID NO:5, SEQ ID NO:7, the complement of SEQ ID NO:7, SEQ ID NO:9, the complement of SEQ ID NO:9, SEQ ID NO:11, the complement of SEQ ID NO:11, SEQ ID NO:13, and the complement of SEQ ID NO:13; and

15 (b) modifying one or more nucleotides in said sequence to another nucleotide, deleting one or more nucleotides in said sequence, or adding one or more nucleotides to said sequence.

143. The method of claim 142, wherein the variant is optimized for expression in a host cell.

20 144. The method of claim 143, wherein the host cell is selected from the group consisting of a bacterial cell, a fungal cell, a plant cell, and an animal cell.

25 145. The method of claim 142, wherein the modifications are introduced by a method selected from the group consisting of error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, ligation reassembly, GSSM and any combination thereof.

146. The method of claim 142, wherein the modifications are introduced by error-prone PCR.

30 147. The method of claim 142, wherein the modifications are introduced by shuffling.

148. The method of claim 142, wherein the modifications are introduced by oligonucleotide-directed mutagenesis.
149. The method of claim 142, wherein the modifications are introduced by assembly PCR.
- 5 150. The method of claim 142, wherein the modifications are introduced by sexual PCR mutagenesis.
151. The method of claim 142, wherein the modifications are introduced by in vivo mutagenesis.
- 10 152. The method of claim 142, wherein the modifications are introduced by cassette mutagenesis.
153. The method of claim 142, wherein the modifications are introduced by recursive ensemble mutagenesis.
154. The method of claim 142, wherein the modifications are introduced by exponential ensemble mutagenesis.
- 15 155. The method of claim 142, wherein the modifications are introduced by site-specific mutagenesis.
156. A computer readable medium having stored thereon a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, the complement of SEQ ID NO:1, SEQ ID NO:3, the complement of SEQ ID NO:3, SEQ ID NO:5, the complement of SEQ ID NO:5, SEQ ID NO:7, the complement of SEQ ID NO:7, SEQ ID NO:9, the complement of SEQ ID NO:9, SEQ ID NO:11, the complement of SEQ ID NO:11, SEQ ID NO:13, and the complement of SEQ ID NO:13 and sequences substantially identical thereto.
- 20 157. A computer readable medium having stored thereon a nucleic acid sequence selected from the group consisting of a polypeptide sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14, and sequences substantially identical thereto.
- 25 158. A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a nucleic acid sequence selected from
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the group consisting of SEQ ID NO:1, the complement of SEQ ID NO:1, SEQ ID NO:3, the complement of SEQ ID NO:3, SEQ ID NO:5, the complement of SEQ ID NO:5, SEQ ID NO:7, the complement of SEQ ID NO:7, SEQ ID NO:9, the complement of SEQ ID NO:9, SEQ ID NO:11, the complement of SEQ ID NO:11, SEQ ID NO:13, and the complement of SEQ ID NO:13 and sequences substantially identical thereto.

159. A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a nucleic acid sequence selected from the group consisting of a polypeptide sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14, and sequences substantially identical thereto.

160. The computer system of claim 159, further comprising a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon.

161. The computer system of claim 159, wherein the sequence comparison algorithm comprises a computer program which indicates polymorphisms.

162. The computer system of claim 159, further comprising an identifier which identifies features in said sequence.

163. A method for comparing a first sequence to a reference sequence comprising:

(a) reading the first sequence and the reference sequence through use of a computer program which compares sequences; and

(b) determining differences between the first sequence and the reference sequence with the computer program, wherein the first sequence is a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, the complement of SEQ ID NO:1, SEQ ID NO:3, the complement of SEQ ID NO:3, SEQ ID NO:5, the complement of SEQ ID NO:5, SEQ ID NO:7, the complement of SEQ ID NO:7, SEQ ID NO:9, the complement of SEQ ID NO:9, SEQ ID NO:11, the complement of SEQ ID NO:11, SEQ ID NO:13, and the complement of SEQ ID NO:13 and sequences substantially identical thereto

164. A method for comparing a first sequence to a reference sequence comprising:

- (a) reading the first sequence and the reference sequence through use of a computer program which compares sequences; and
 - (b) determining differences between the first sequence and the reference sequence with the computer program, wherein the first sequence is a polypeptide sequence having the amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14, and sequences substantially identical thereto.
165. The method of claim 163 or 164, wherein determining differences between the first sequence and the reference sequence comprises identifying polymorphisms.
166. A method for identifying a feature in a sequence comprising:
- (a) reading the sequence through the use of a computer program which identifies features in sequences; and
 - (b) identifying features in the sequences with the computer program wherein the sequence is a nucleic acid sequence having an amino acid sequence selected from the group consisting of SEQ ID NO:1, the complement of SEQ ID NO:1, SEQ ID NO:3, the complement of SEQ ID NO:3, SEQ ID NO:5, the complement of SEQ ID NO:5, SEQ ID NO:7, the complement of SEQ ID NO:7, SEQ ID NO:9, the complement of SEQ ID NO:9, SEQ ID NO:11, the complement of SEQ ID NO:11, SEQ ID NO:13, and the complement of SEQ ID NO:13 and sequences substantially identical thereto.
167. A method for identifying a feature in a sequence comprising:
- (a) reading the sequence through the use of a computer program which identifies features in sequences; and
 - (b) identifying features in the sequences with the computer program, wherein the first sequence is a polypeptide sequence having the amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14, and sequences substantially identical thereto.
168. A method to identify a phytate sequence comprising analyzing an amino acid sequence for the occurrence of a first region consisting of RHGVRXaaPT (SEQ ID NO:17) and a second region consisting of WPXaaWPV (SEQ ID NO:18), wherein

the first and second region are separated by 13 amino acids, wherein Xaa can be any amino acid.

169. The method of claim 168, wherein the first and the second region are separated by 10, 11, 12, 14, 15, or 16 amino acids.

5 170. An isolated nucleic acid encoding a phytase protein having an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14 optimized for codon usage in an organism.

10 171. The nucleic acid of claim 170 optimized for expression in a bacterium, a plant, a fungus or an animal.

172. The nucleic acid of claim 171 optimized for codon usage in an organism selected from the group consisting of *S. pombe*, *S. cerevisiae*, *Pichia pastoris*, *Psuedomonas sp.*, *E. coli*, *Streptomyces sp.*, *Bacillus sp.*, *Lactobacillus sp.*